

# HUMAN xiap

SEQ ID NO:4 a

SENTENCES

a K T C V P A D I N K E E F F V E E F F N R

a L K T F A N F P S G S P V S A S T L A R

a A G F L Y T G E G D T V R C F S C H A A

a V D R W Q Y G D S A V G R H R K V S P N

a C R F I N G F Y L E N S A T Q S T N S C

**FIG. 1 (PAGE 1 OF 7)**

# HUMAN xiap

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361 atccagaatggtcagtagacaaagtgaataactatctgtggaagcagagatcatttgcctta
a I Q N G Q Y K V E N Y L G S R D H F A L
421 gacaggccatctgagacacatgcagactatcttttgagaactgggcagggtttagatata
a D R P S E T H A D Y L L R T G Q V V D I
481 tcagacacatataccgaggaaccctgccatgtattgtgaagaagctagattaaagtcc
a S D T I Y P R N P A M Y C E E A R L K S
541 ttccagaactggccagactatgctcacctaaccacaaagagagtagcaagtgtggactc
a F Q N W P D Y A H L T P R E L A S A G L
601 tactacacaggtattggtgaccaagtgcagtgcttttgtgtgtggaactgaaaaat
a Y Y T G I G D Q V Q C F C C G G K L K N
661 tgggaaccttgtgatcgctgcctggtcagaacacagcgacactttcctaattgcttcttc
a W E P C D R A W S E H R R H F P N C F F
720

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FIG. 1 (PAGE 2 OF 7)

# HUMAN xiap

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721  gttttggccggaatcttaataattcgaagtgaatctgatgctgtgagttctgataggaat 780
a    V L G R N L N I R S E S D A V S S D R N -
781  ttcccaaatcaacaaatcttccaagaatacccatccatggcagattatgaagcacggatc 840
a    F P N S T N L P R N P S M A D Y E A R I -
841  ttacttttgggacatggatatactcagttaacaaggagcagcttgcaagagctggattt 900
a    F T F G T W I Y S V N K E Q L A R A G F -
901  tatgctttaggtgaaggtgataaaagtgtcttccactgtggaggaggctaaactgat 960
a    Y A L G E G D K V K C F H C G G L T D -
961  tggaagcccagtgaaagacccttggaacaacatgctaaatgggtatccagggtgcaaatat 1020
a    W K P S E D P W E Q H A K W Y P G C K Y -
1021 ctgttagaacagaaggacaagaatatataaacaatatccatttaactcattcacttgag 1080
a    L L E Q K G Q E Y I N N I H L T H S L E -

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FIG. 1 (PAGE 3 OF 7)

# HUMAN xiap

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1081 gagtgtctggttaagaactactgagaaaaacaccatcactaactagaagaattgatatacc 1140
      E C L V R T T E K T P S L T R R I D D T -
1141 atcttccaaaatcctatggtacaagaagctatacgaatgggttcagtttcaaggacatt 1200
      I F Q N P M V Q E A I R M G F S F K D I -
1201 aagaaaaataatggaggaaaaaattcagatatctgggagcaactataaatacacttgaggtt 1260
      K K I M E E K I Q I S G S N Y K S L E V -
1261 ctggttgcagatctagtgaatgctcagaaaagacagtatgcaagatgagtcagtcagact 1320
      L V A D L V N A Q K D S M Q D E S S Q T -
1321 tcattacagaaaagagattagtactgaagagcagctaaggcgctgcaagaggagaagctt 1380
      S L Q K E I S T E E Q L R R L Q E E K L -
1381 tgcaaaaatctgtatggatagaaaataattgctatcgttttgttccttgtggacatctagtc 1440

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FIG. 1 (PAGE 4 OF 7)

# HUMAN xiap

a	C	K	I	C	M	D	R	N	I	A	I	V	F	V	P	C	G	H	L	V	-
	acttgtaacaatgtgctgaagcagttgacaagtgccccatgtgctacacagtcattact																				1500
1441	-----+																				
a	T	C	K	Q	C	A	E	A	V	D	K	C	P	M	C	Y	T	V	I	T	-
	ttcaagcaaaaaatttttatgtctttaacttaactctatagtaggcattgttattgttct																				1560
1501	-----+																				
a	F K Q K I F M S *																				-
	tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaaattccat																				1620
1561	-----+																				
a	tagcatttgctaccaagtaggaaaaaaatgtacatggcagtggttttagttggcaatata																				1680
1621	-----+																				
a	atctttgaaatttcttgatttttcagggtattagctgtattatccatttttttactgtta																				1740
1681	-----+																				
a	tttaattgaaaccatagactaagaataaagaagcatcatactataactgaacacaatgtgt																				1800
1741	-----+																				
a																					-

FIG. 1 (PAGE 5 OF 7)





# HUMAN hiap-1

SEQ ID NO:5

1 TCCTTGAGATGATCAGTATAGGATTTAGGATCTCCATGTTGGAACCTCTAAATGCATAGA  
60

C

61 AATGGAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTAATACTGATAAAA  
120

C

121 GCAAAGCCATGCACAAACTACCTCCCTAGAGAAAGGCTAGTCCCTTTCTTCCCCATTC  
180

C

181 ATTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAAATTTGATGAAAAGCGCCA  
240

SEQ ID NO:6 C

M N I V E N S I F L S N L M K S A N  
241 ACACGTTTGAAC TGAATAACGACTTGTCAATGTGAACGTACCGAATGTCTACGTATTCCA  
300

C

T F E L K Y D L S C E L Y R M S T Y S T  
301 CTTTCCCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGGTTCATTACA  
360

C

F P A G V P V S E R S L A R A G F Y Y T

FIG. 2 (PAGE 1 OF 8)





# HUMAN hiap-1

721	C	CATGGCCATTGACTTTCTGTCGCCAACAGATCTGGCAGCAGCAGGCTTTTACTACATAG	780
		W P L T F L S P T D L A R A G F Y Y I G -	
781		GACCTGGAGACAGAGTGGCTTGTGCTTGGTGGTGGAAATTGAGCAATTGGGAACCGA	840
		P G D R V A C F A C G G K L S N W E P K -	
841	C	AGGATAATGCTATGTCAGAACACCTGAGACATTTTCCCAAATGCCCATTTATAGAAAATC	900
		D N A M S E H L R H F P K C P F I E N Q -	
901		AGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGACACATGCAGCCCC	960
		L Q D T S R Y T V S N L S M Q T H A A R -	
961	C	GCTTTAAACATTCTTAACTGGCCCTCTAGTGTCTAGTTAATCCTGAGCAGCTTGCAA	1020
		F K T F F N W P S S V L V N P E Q L A S -	
1021	C	GTGCGGGTTTTTATTATGTGGGTAACAGTGATGATGTCAAAATGCTTTTGTGTGATGTG	1080
		A G F Y Y V G N S D D V K C C F C C D G G -	

FIG. 2 (PAGE 3 OF 8)

# HUMAN hiap-1

1081	GACTCAGGTGTGGGAATCTGGAGATGATCCATGGGTCAACATGCCAAGTGTTCCAA	1140
C	L R C W E S G D D P W V Q H A K W F P R -	
1141	GGTGTGAGTACTTGATAAGAAATTAAGGACAGGAGTTTCATCCGTCAGTTCAAGCCAGTT	1200
C	C E Y L I R I K G Q E F I R Q V Q A S Y -	
1201	ACCCATCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCCCAGGAGATGAAATGCAG	1260
C	P H L L E Q L L S T S D S P G D E N A E -	
1261	AGTCATCAATTATCCATTGGAACTGGAGAAGACCATTCAAGAAGATGCAATCATGATGA	1320
C	S S I I H L E P G E D H S E D A I M M N -	
1321	ATACTCCTGTGATTAAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCCTGGTAAACAGA	1380
C	T P V I N A A V E M G F S R S L V K Q T -	
1381	CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAAATTATAGACTAGTCAATGATCTTGTGT	1440
C	V Q R K I L A T G E N Y R L V N D L V L -	

FIG. 2 (PAGE 4 OF 8)

# HUMAN hiap-1

1441	TAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGAGAGAGAAAGCAACTGAGG	1500
C	D L L N A E D E I R E E E R A T E E -	
1501	AAAAAGAATCAAAATGATTATTATTAATCCGGAAGAATAGAAATGGCACTTTTTCACACATT	1560
C	K E S N D L L L I R K N R M A L F Q H L -	
1561	TGACTTGTGTAAATCCCAATCCTGGATAGTCTACTAACTGCCGGAATTATTATGAACAAG	1620
C	T C V I P I L D S L L T A G I I N E Q E -	
1621	AACATGATGTTATTAACAGAAGACACAGACGCTTTACAAGCAAGAGAACTGATTGATA	1680
C	H D V I K Q K T Q T S L Q A R E L I D T -	
1681	CGATTTAGTAAAGGAAATATTGCAGCCACTGTATTCAGAAACTCTCTGCAAGAAAGCTG	1740
C	I L V K G N I A A T V F R N S L Q E A E -	
1741	AAGCTGTGTATATGAGCATTTATTGTGTCAACAGGACATATAATATATTCACACAGAAG	1800
C	A V L Y E H L F V Q Q D I K Y I P T E D -	

FIG. 2 (PAGE 5 OF 8)

# HUMAN hiap-1

1801	ATGTTTCAGATCTACCAGTGAAGAACAATTGCGGAGACTACCAGAAGAAACAATGTA	1860
	V S D L P V E E Q L R R L P E E R T C K -	
1861	AAGTGTGTATGGACAAAGAAGTGTCCTAGTGTATTCCCTTGTGGTCATCTAGTAGTAT	1920
	V C M D K E V S I V F I P C G H L V V C -	
1921	GCAAAGATTGTGCTCCTTCTTAAGAAAGTGTCCTATTTGTAGGAGTACAAATCAAGGGTA	1980
	K D C A P S L R K C P I C R S T I K G T -	
1981	CAGTTCGTACATTTCTTCATGAAGAAGAACCAACATCGTCTAAACTTTAGAAATTAAT	2040
	V R T F L S *	
2041	TTATTAAATGTATTATAACTTTAACTTTTATCCTAATTGGTTTCCTTAAATTTTATT	2100
	TATTACAAC TCAAAAACATTGTTTGTGTAAACATATTTATATATGTATCTAAACCATA	2160
2101		

FIG. 2 (PAGE 6 OF 8)



## HUMAN hiap-1

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2521  CAGTGTCCTATACATCGAAGGTGTCATATATGTTGAATCACATTTAGGACATGGTGT 2580
      -----+-----+-----+-----+-----+-----+
      -
2581  TTTTATAAGAAATCTGTGAGXAAAAATTTAATAAAGCAACCXAAATTACTCTTAAAAAA 2640
      -----+-----+-----+-----+-----+-----+
      -
2641  AAAAAAAAAAAAACTCGAGGGGCCCCGTACCAAT 2676
      -----+-----+-----+-----+-----+
      -
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FIG. 2 (PAGE 8 OF 8)

# HUMAN hiap-2

SEQ ID NO:7

1 TTAGGTTACCTGAAAGAGTTACTACAACCCCAAGAGTTGTGTTCTAAGTAGTATCTTGG  
 60

a

61 TAAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAAGAAAG  
 120

a

121 TGTAATAATTCTACATAAGAGTCTATCATTTGATTCTTTTGTGGTGGAAATCTTAGTT  
 180

a

181 CATGTGAAGAAATTCATGTGAATGTTTAGCTATCAACAGTACTGTCACCTACTCATG  
 240

a

241 CACAAAAGTGCCTCCCAAGACTTTTCCCAGGTCCTCGTATCAAAACATTAAGAGTATA  
 300

SEQ ID NO:8 a

H K T A S Q R L F P G P S Y Q N I K S I  
 301 ATGGAAGATAGCAGCATCTTGTTCAGATTGGACAAACAGCAACAAACAAATGAAGTAT  
 360

a

M E D S T I L S D W T N S N K Q K M K Y

FIG. 3 (PAGE 1 OF 7)



# HUMAN hiap-2

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361  GACTTTCCCTGTGAACTCTACAGAAATGTCTACATATTCAACTTCCCCCGGGTGCCT 420
a    D F S C E L Y R M S T Y S T F P A G V P -
421  GTCTCAGAAAGGAGTCTTGCTCGTGGTGTCTTTTATTATATACTGGTGTGAATGACAAAGGTC 480
a    V S E R S L A R A G F Y Y T G V N D K V -
481  AAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAACACTAGGAGACAGTCCCTATTCAA 540
a    K C F C C G L M L D N W K L G D S P I Q -
541  AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAATCTGGTTTCAGCTAGTCTG 600
a    K H K Q L Y P S C S F I Q N L V S A S L -
601  GGATCCACCTCTAAGAAATACGCTCCCAATGAGAAACAGTTTGGCACATTCAATCTCTCCC 660
a    G S T S K N T S P M R N S F A H S L S P -
661  ACCTTGGAACATAGTAGCTTGTTTCAGTGGTCTTACTCCAGCCTTCTCTCAACCCCTCTT 720
a    T L E H S S L F S G S Y S S L P P N P L -

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FIG. 3 (PAGE 2 OF 7)

# HUMAN hiap-2

721	AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG	780
a	N S R A V E D I S S R T N P Y S Y A M	-
801	AGTACTGAAGAAGCCAGATTCTTACCTACCATATGTGGCCATTAACTTTTGTGCACCA	840
a	S T E E A R F L T Y H M W P L T F L S P	-
841	TCAGAATTGGCAAGAGCTGTTTTATATATAGGACCTGGAGATAGGCTAGCCTGCTTT	900
a	S E L A R A G F Y Y I G P G D R V A C F	-
901	GCCTGTGTGGGAGCTCAGTAACTGGGAACCAAGGATGCTATGTCAGAACACCGG	960
a	A C G G K L S N W E P K D D A M S E H R	-
961	AGGCATTTCCCAACTGTCCATTTTGGAAAATTCTCTAGAAACTCTGAGGTTAGCATT	1020
a	R H F P N C P F L E N S L E T L R F S I	-
1021	TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTATGTACTGGCCATCT	1080
a	S N L S M Q T H A A R M R T F M Y W P S	-

FIG. 3 (PAGE 3 OF 7)

# HUMAN hiap-2

1081	AGTGTCCAGTTCAGCCTGAGCAGCTTGCAAGTGCTGGTTTATATATGTGGTCGCAAT	1140
a	S V P V Q P E Q L A S A G F Y Y V G R N	-
1141	GATGATGCAAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTGGGAATCTGGAGATGAT	1200
a	D D V K C F G C D G G L R C W E S G D D	-
1201	CCATGGGTAGAACATGCCAAGTGGTTTCCCAAGGTGTGAGTTCTTGATACGAATGAAAGGC	1260
a	P W V E H A K W F P R C E F L I R M K G	-
1261	CAAGAGTTTGGTTGATGAGATTCAAGGTAGATATCCCTCATCTTCTTGACACAGCTGTTGTCA	1320
a	Q E F V D E I Q G R Y P H L L E Q L L S	-
1321	ACTTCAGATACCACTGGAGAGAAATGCTGACCCACCAATTATTCATTTTGGACCTGGA	1380
a	T S D T T G E E N A D P P I I H F G P G	-
1381	GAAAGTTCTCAGAAGATGCTGTCATGATGAATACACCTGTGGTTAAATCTGCCCTTGGA	1440
a	E S S S E D A V M M N T P V V K S A L E	-

FIG. 3 (PAGE 4 OF 7)

# HUMAN hiap-2

1441	ATGGGCTTAA	TAGAGACCTGGTGA	AAACACAGTTCTA	AGTAAAAATCCTG	ACAACTGGA	1500
a	M G F N R D L V K Q T V L S K I L T T G	-				
1501	GAGAACTATA	AAACAGTTAATG	ATATTGTGTCAG	CACCTTCTTAAT	GCTGAAGATGA	1560
a	E N Y K T V N D I V S A L L N A E D E K	-				
1561	AGAGAAAGAG	AAGGAAAAACA	AGCTGAAGAAAT	GGCATCAGATG	ATTGTTCATTA	1620
a	R E E E K E K Q A E E M A S	D D L S L I	-			
1621	CGGAAGAACAG	AATGGCTCTCTT	TCAACAATTGAC	ATGTGTGCTTC	CTATCCTGGATA	1680
a	R K N R M A L F Q Q L T C V L P I L D N	-				
1681	CTTTTAAAGG	CCAATGTAATT	ATAAACAGGA	ACATGATATT	TATAACAAAA	1740
a	L L K A N V I N K Q E H D I I K Q K T Q	-				
1741	ATACCTTTAC	AAGCAGAGAACT	GATTGATACCAT	TGTTGGTTAA	AGGAAATGCTG	1800
a	I P L Q A R E L I D T I W V K	G N A A A	-			

FIG. 3 (PAGE 5 OF 7)

# HUMAN hiap-2

1801	AACATCTTCAAAACTGTCTAAAAGAAATTGACTCTACATTGTATAAGAACTTATTGTG	1860
a	N I F K N C L K E I D S T L Y K N L F V	-
1861	GATAAGAAATATGAAGTATATTCCACAGAGAAGATGTTTCAGGCTGTCACTGGAAGAACAA	1920
a	D K N M K Y I P T E D V S G L S L E E Q	-
1921	TTGAGGAGGTTGCAAGAAGAACGAACTTGTAAGTGATGACAAAGAAGTTCTCTGT	1980
a	L R R L Q E E R T C K V C M D K E V S V	-
1981	GTATTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCCCTTCTCTAAGAAA	2040
a	V F I P C G H L V V C Q E C A P S L R K	-
2041	TGCCCTATTTCAGGGGTATAATCAAGGGTACTGTTTCGTACATTCTCTCTTAAAGAAA	2100
a	C P I C R G I I K G T V R T F L S *	-
2101	ATAGTCTATATTTAACCTGCATATAAAGGCTCTTAAATAATGTTGAACACTTGAAGCC	2160
a		-

FIG. 3 (PAGE 6 OF 7)

# HUMAN hiap-2

2161	ATCTAAAGTAAAAAGGAATTATGAGTTTTTCAATTAGTAACATTCAATGTTCTAGTCTGC	2220
a	-	-
2221	TTTGGTACTAATAATCTTTGTTCTGAAAAGATGGTATCATATATTAACTCTTAATCTGTT	2280
a	-	-
2281	TATTACAAGGGAAGATTATGTTTGGTGAACATATATAGTATGTGTACCTAAGGG	2340
a	-	-
2341	AGTAGCGTCXCTGCTTGTATGCATCATTTTCAGGAGTTACTGGATTTGTTGTTCTTTCAG	2400
a	-	-
2401	AAAGCCTTTGAAXACTAAATTATAGTGAGTAAAGAACTGGAAACCAGGAACCTCTGGAGTT	2460
a	-	-
2461	CATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTTGTTTAAATAAGGA	2520
a	-	-
2521	TTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTCCTTAAAAAG	2580
a	-	-

FIG. 3 (PAGE 7 OF 7)



# MOUSE xiap

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361  GCTGTTGGAAGACACAGGAGAAATATCCCCAAATTCAGATTATCAATGGTTTATTTT 420
      A V G R H R R I S P N C R F I N G F Y F -
421  GAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAATGGCCAGTACAAATCTGAA 480
      E N G A A Q S T N P G I Q N G Q Y K S E -
481  AACTGTGTGGGAAATAGAAATCCTTTTGCCCTTGACAGGCCACCTGAGACTCATGCTGAT 540
      N C V G N R N P F A P D R P P E T H A D -
541  TATCTCTTGAGAACTGGACAGGTTGTAGATATTTTCAGACACCATATACCCGAGGAACCT 600
      Y L L R T G Q V V D I S D T I Y P R N P -
601  GCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTCAGAACTGCCCGGACTATGCTCAT 660
      A M C S E E A R L K S F Q N W P D Y A H -
661  TTAACCCCCAGAGAGTTAGCTAGTGGCTGCTTACTACACAGGGGCTGATGATCAAGTG 720
      L T P R E L A S A G L Y Y T G A D D Q V -

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FIG. 4 (PAGE 2 OF 6)



# MOUSE xiap

721	CAATGCTTTTGTGGGGAAACTGAAAAATTGGGAACCTGTGATCGTGCTCGTCA	780
a	Q C F C C G G K L K N W E P C D R A W S	-
781	GAACACAGGAGACACTTCCCAATGCTTTTGTGTTGGGCCGGAACGTTAATGTTCCA	840
a	E H R R H F P N C F F V L G R N V N V R	-
841	AGTGAATCTGGTGTGAGTTCTGATAGGAATTCCCCAAATTCACAAACTCTCCAAGAAAT	900
a	S E S G V S S D R N F P N S T N S P R N	-
901	CCAGCCATGGCAGAAATATGAAGCACGGATCGTTACTTTTGGACATGGATATACTCAGTT	960
a	P A M A E Y E A R I V T F G T W I Y S V	-
961	AACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAG	1020
a	N K E Q L A R A G F Y A L G E G D K V K	-
1021	TGCTTCCACTGTGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGACCAG	1080
a	C F H C G G G L T D W K P S E D P W D Q	-

FIG. 4 (PAGE 3 OF 6)

# MOUSE xiap

1081	CATGCTAAGTGTACCCAGGTGCAATAACCTATTGGATGAGAAGGGCAAGATATATA	1140
a	H A K C Y P G C K Y L L D E K G Q E Y I	-
1141	AATAATATTCAATTAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAAACA	1200
a	N N I H L T H P L E E S L G R T A E K T	-
1201	CCACCGCTAACTAAAAATCGATGATACCATCTTCCAGAAATCCTATGGTGCAAGAAGCT	1260
a	P P L T K K I D D T I F Q N P M V Q E A	-
1261	ATACGAATGGGATTAGCTTCAAGGACCTTAAGAAAAACAATGGAAGAAAAATCCAAACA	1320
a	I R M G F S F K D L K K T M E E K I Q T	-
1321	TCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTCAGATCTTGTGAGTGCTCAGAAA	1380
a	S G S S Y L S L E V L I A D L V S A Q K	-
1381	GATAATACGAGGATGAGTCAAGTCAAACTTCAATTCAGAAAGACATTAGTACTGAAGAG	1440
a	D N T E D E S S Q T S L Q K D I S T E E	-

FIG. 4 (PAGE 4 OF 6)

# MOUSE xiap

1441	CAGCTAAGGCGCCTACAAGAGGAGAAGCTTCCAAATCTGTATGATAGAAATATTGCT	1500
a	Q L R R L Q E E K L S K I C M D R N I A	-
1501	ATCGTTTTTTTCCCTGTGGACATCTGGCCACTTGTAACAGTGTGCAGAGCAGTTGAC	1560
a	I V F F P C G H L A T C K Q C A E A V D	-
1561	AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAATTTTATGTCTTAGTGG	1620
a	K C P M C Y T V I T F N Q K I F M S *	-
1621	GGCACCACATGTTATGTTCTTCTTGCTCTAATGAATGTGTAATGGAGCGAACTTTAAG	1680
a		-
1681	TAATCCTGCATTTGCAATTCATTAGCATCCCTGCTGTTTCCAAATGGAGACCAATGCTAAC	1740
a		-
1741	AGCACTGTTTCCGCTAAACATTCAATTTCTGGATCTTTTCGAGTTATCAGCTGTATCATT	1800
a		-

FIG. 4 (PAGE 5 OF 6)

# MOUSE xiap

1801	TAGCCAGTGT	TTTACTCGATTGAAACCTTAGACAGAGAAAGCATT	TTTATAGCTTTTCACAT	1860
a				-
1861	GTATATTGGTAGTACACTGACTTGATT	TCTATATGTAAGTGAATTCATCACCCTGCATGTT		1920
a				-
1921	TCATGCCCTTTTGCA	TAAAGCTTAACAAATGGAGTGTTCTGTATAAGCATGGAGATGTGATG		1980
a				-
1981	GAATCTGCCCCAATGACTTTAA	TGGCTTATTGTAAACACGGAAAGAACTGCCCCCACGCTG		2040
a				-
2041	CTGGGAGGATAAAGATTGTTTAGATGCTCACTTCTGTGTTTAGGATTCTGCCCATTTA			2100

FIG. 4 (PAGE 6 OF 6)



# M-hiap-1

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CACAGAAAGTTGTACCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGCTG
421 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 480
H R K L Y P S C N F V Q T L N P A N S L -

GAAGCTAGTCCTCGGCCTTCTCTTCCACGGCGATGAGCACCATGCCCTTGAGCTTT
481 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 540
E A S P R P S L P S T A M S T M P L S F -

GCAAGTTCGAGAAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCTCCAGACCT
541 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 600
A S S E N T G Y F S G S Y S S F P S D P -

GTGAACTTCGAGCAAAATCAAGATTGTCCTGCTTTGAGCACAAAGTCCCTACCATTGCA
601 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 660
V N F R A N Q D C P A L S T S P Y H F A -

ATGAACACAGAGAAGGCCAGATTACTCACCTATGAAACATGGCCATTGTCTTTCTGTCA
661 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 720
M N T E K A R L L T Y E T W P L S F L S -

CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGACCTGGAGATAGAGTGCCCTGC
721 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 780
P A K L A K A G F Y Y I G P G D R V A C -

```

FIG. 5 (PAGE 2 OF 6)

# M-hiap-1

```

781 TTTGCGTGGGAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC
-----+-----+-----+-----+-----+-----+
F A C D G K L S N W E R K D D A M S E H - 840

841 CAGAGGCATTTCCCCAGCTGTCGTTCTTAAAAGACTTGGTCAGTCTGCTTCGAGATAC
-----+-----+-----+-----+-----+-----+
Q R H F P S C P F L K D L G Q S A S R Y - 900

901 ACTGCTCTTAACCTGAGCATGCAGACACAGCCCGTATTAGAACATTCTCTAACTGG
-----+-----+-----+-----+-----+-----+
T V S N L S M Q T H A A R I R T F S N W - 960

961 CCTTCTAGTGCAC TAGTTCATTC CAGGA ACTTGCAAGT CGGGCTTTATTATACAGGA
-----+-----+-----+-----+-----+-----+
P S S A L V H S Q E L A S A G F Y Y T G - 1020

1021 CACAGTGATGTCAAGTGTATTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA
-----+-----+-----+-----+-----+-----+
H S D D V K C L C C D G G L R C W E S G - 1080

1081 GATGACCCCTGGTGGAACATGCCAAGTGGTTCCAAGGTGTGAGTACTTGCTCAGAATC
-----+-----+-----+-----+-----+-----+
D D P W V E H A K W F P R C E Y L L R I - 1140

1141 AAAGGCCAAGAATTTGTCAGCCCAAGTTC AAGCTGGCTATCCTCATCTACTTGAGCAGCTA
-----+-----+-----+-----+-----+-----+
K G Q E F V S Q V Q A G Y P H L L E Q L - 1200

```

FIG. 5 (PAGE 3 OF 6)

# M-hiap-1

1201	TTATCTACGTCAGACTCCCAGAAGATGAGAATGCAGACGCAGCAATCGTGCAATTTGGC	1260
	L S T S D S P E D E N A D A A I V H F G	
1261	CCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCCTGTGGTTAAAGCAGCCTTG	1320
	P G E S S E D V V M M S T P V V K A A L	
1321	GAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGCTTCAGTGGCAGATCCTGGCCACT	1380
	E M G F S R S L V R Q T V Q W Q I L A T	
1381	GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG	1440
	G E N Y R T V S D L V I G L L D A E D E	
1441	ATGAGAGAGGAGCAGATGGAGCAGCGCGCCGAGAGGAGTCAAGATGATCTAGCACTA	1500
	M R E E Q M E Q A A E E E E S D D L A L	
1501	ATCCGGAAGAACAAATGGTGCTTTTCCAACATTTGACGTGTGTGACACCAATGCTGTAT	1560
	I R K N K M V L F Q H L T C V T P M L Y	

FIG. 5 (PAGE 4 OF 6)



# M-hiap-1

1561	TGCCCTCCTAAGTGCAAGGCCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA	1620
	C L L S A R A I T E Q E C N A V K Q K P	-
1621	CACACCTTACAAGCAAGCACACTGATTGATACTGTGTAGCAAAAGGAAACACTGCAGCA	1680
	H T L Q A S T L I D T V L A K G N T A A	-
1681	ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCCTCGTTATACAGAGATATTTGTG	1740
	T S F R N S L R E I D P A L Y R D I F V	-
1741	CAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG	1800
	Q Q D I R S L P T D D I A A L P M E E Q	-
1801	TTGCGGCCCTCCCGAGGACAGAAATGTGTAAAGTGTGTATGGACCGAGAGGTATCCATC	1860
	L R P L P E D R M C K V C M D R E V S I	-
1861	GTGTTCAATCCCTGTGGCCATCTGGTCGTGTGCAAAAGACTGCGCTCCCTCTCTGAGGAAG	1920
	V F I P C G H L V V C K D C A P S L R K	-

FIG. 5 (PAGE 5 OF 6)

# M-hiap-1

1921	TGTCCCATCTGTAGAGGACCATCAAGGCACAGTGGCCACATTTCTCTCTGAAACAAGA	1980
	C P I C R G T I K G T V R T F L S *	-
1981	CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACCTGTCACTCCCAGTTCCAT	2040
2041	TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACACACAAATATAAACAT	2100
2101	GAAAAACTTTTGTCTGAAGTCAAGAATGAATGAAATTAATAATAATTTAATTGGT	2160
2161	TTCCCTTAAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTTCTGTAAACATATTACA	2220
2221	TACTACCTGCATCTAAAGTATTTCATATATATTCATATATTCAGATGTCATGAGAGGGTTT	2280
2281	TGTTCTTGTTCCCTGAAAAGCTGGTTTATCATCTGTATCAGCATATATACTGCGCAACGGGCAG	2340
2341	GGCTAGAAATCCATGAACCAAGCTGCAAAGATCTCACGCTAAATAAGCGGAAAGATTGG	2400
2401	AGAAACGAAAGGAAAATTCTTTCCCTGTCCAATGTATACTCTTCAGACTAATGACCCCTTCC	2460
2461	TATCAAGCCTTCTA	
	-----+----- 2474	

FIG. 5 (PAGE 6 OF 6)



# M-hiap-2

```

421  GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAATAATGTCTCTGTGAAAAGTAG
      T L L S A S L Q S P S K N M S P V K S R - 480
481  ATTTGCACATTTCGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
      F A H S S P L E R G G I H S N L C S S P - 540
541  TCTTAATTCTAGAGCAGTGGAAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
      L N S R A V E D F S S R M D P C S Y A M - 600
601  GAGTACAGAAGAGGCCAGATTCTTACTTACAGTATGTGGCCTTAAAGTTTCTGTCACC
      S T E E A R F L T Y S M W P L S F L S P - 660
661  AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGCCCTGGAGACAGGGTGGCCTGTTT
      A E L A R A G F Y Y I G P G D R V A C F - 720
721  TGCCTGTGTGGAAACTGAGCAACTGGGAACCAAGGATTATGCTATGTCAGAGCACCG
      A C G G K L S N W E P K D Y A M S E H R - 780

```

FIG. 6 (PAGE 2 OF 6)

## M-hiap-2

781	CAGACATTTTCCCACTGTCATTCTTGAAATACTTCAGAAACACAGAGGTTTAGTAT	840
	R H F P H C P F L E N T S E T Q R F S I	
841	ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC	900
	S N L S M Q T H S A R L R T F L Y W P P	
901	TAGTGTTCCTGTTCAAGCCGAGCAGCTTGCAAGTCTGATTCTATTACGTGGATCGCAA	960
	S V P V Q P E Q L A S A G F Y Y V D R N	
961	TGATGATGTCAGTGCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA	1020
	D D V K C L C C D G G L R C W E P G D D	
1021	CCCCTGGATAGAACACGCGCAAAATGGTTTCCAAGGTGTGAGTTCTTGATACGGATGAAGGG	1080
	P W I E H A K W F P R C E F L I R M K G	
1081	TCAGGAGTTTGTGATGAGATTCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGTGTC	1140
	Q E F V D E I Q A R Y P H L L E Q L L S	

FIG. 6 (PAGE 3 OF 6)

## M-hiap-2

```

1141 CACTTCAGACACCCAGGAGAAATGCTGACCCCTACAGACAGTGCGCATTTGG + 1200
      T S D T P G E E N A D P T E T V V H F G -
1201 CCCTGGAGAAAGTTTCGAAAGATGTCGTCATGATGAGCACGCCCTGTGGTTAAAGCAGCCTT + 1260
      P G E S S K D V V M M S T P V V K A A L -
1261 GGAATGGGCTTCAGTAGAGCCTGGTGAGACAGACGTTTCAGCGGCAGATCCTGGCCAC + 1320
      E M G F S R S L V R Q T V Q R Q I L A T -
1321 TGGTGAGAACTACAGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA + 1380
      G E N Y R T V N D I V S V L L N A E D E -
1381 GAGAAAGAGAGGAGAGGAAAGACAGACTGAAGAGATGCCATCAGGTGACTTATCACT + 1440
      R R E E E K E R Q T E E M A S G D L S L -
1441 GATTGGAAGAAATAGCCTCTTTCAACAGTTGACACATGTCTTCTATCCTGGA + 1500
      I R K N R M A L F Q Q Q L T H V L P I L D -

```

**FIG. 6 (PAGE 4 OF 6)**

## M-hiap-2

1501	TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAAC	1560
	N L L E A S V I T K Q E H D I I R Q K T	
1561	ACAGATACCCCTTACAAGCAAGAGAGCCTTATTGACACCGTTTTAGTCAAGGGAATGCTGC	1620
	Q I P L Q A R E L I D T V L V K G N A A	
1621	AGCCAACATCTTCAAAAACCTCTCTGAAGGAATTGACTCCACGTTATATGAAAACCTTATT	1680
	A N I F K N S L K G I D S T L Y E N L F	
1681	TGTGGAAGAATATGAAGTATATTCCAACAGAAACGTTTCAGGCTTGTCATTGGAAGA	1740
	V E K N M K Y I P T E D V S G L S L E E	
1741	GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAAGTGTGTATGGACAGAGAGTTTC	1800
	Q L R R L Q E E R T C K V C M D R E V S	
1801	TATTGTGTTTCATTCGGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCTTCTCTAAG	1860
	I V F I P C G H L V V C Q E C A P S L R	

**FIG. 6 (PAGE 5 OF 6)**





# Alignment of BIR (Baculoviral IAP Repeats) Domains

Bacul virus

Cp\_iap

Op\_iap

Human

xiap

hiap1, hiap2

Mouse

m-xiap

Insect

diap

Cydia pomonella

Orgyia pseudotsugata

IAP on X chromosome

two different human IAP genes

mouse homologue of human xiap gene

Drosophila IAP gene, not clearly a homologue of xiap or hiap

FIG. 7

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:11	Op_iap-1	1	kaarLgTttn	WPVqf.l	leps	rMAasGfYI	GrgDeVrCaf	CkveitnWtr	gDdpelDhrr	waPqCpFV	68
SEQ ID NO:14	Cp_iap-1		eevRLnTfEk	WPVsf.l	ispe	tMAknGfYI	GrgDeVrCaf	CkveimrWke	gEdpaadHtk	waPqCpFV	
SEQ ID NO:15	diap-2		eanRLvTfKd	WPnbn.l	lPq	alABAGfYI	nrlDhVkcVw	CngvIakWek	nDnafeeHkr	ffPqCpRV	
SEQ ID NO:16	m-xiap-1		efnRLkTfAn	FPssapvsas		tLArAGfLYt	GegDtVqCfs	ChaaIdrWqy	gDsavgrHrk	IsPnCrFI	
SEQ ID NO:17	xiap-1		efnRLkTfAn	FPssapvsas		tLArAGfLYt	GegDtVrCfs	ChaaIdrWqy	gDsavgrHrk	vsPnCrFI	
SEQ ID NO:18	hiap1-1		elyRMsrYat	FPagvpsas		slArAGfYt	GvndkVkcFg	CglmIdnWkr	gDsptekHtk	lyPscsFI	
SEQ ID NO:19	hiap2-1		elyRMsrYat	FPagvpsas		slArAGfYt	GvndkVkcFg	CglmIdnWkr	gDsptekHtk	lyPscsFI	
SEQ ID NO:20	m-xiap-2		eeRLksFqn	WPdyahltpr		elAaAGLYt	GaddQvqCfc	CggklnWep	cDrawseHrr	hfPnCrFV	
SEQ ID NO:21	xiap-2		eeRLksFqn	WPdyahltpr		elAaAGLYt	GigDqVqCfc	CggklnWep	cDrawseHrr	hfPnCrFV	
SEQ ID NO:22	hiap1-2		eeRLksFqn	WPdyahltpr		elAaAGLYt	GigDqVqCfc	CggklnWep	cDrawseHrr	hfPnCrFV	
SEQ ID NO:23	hiap2-2		eeRLksFqn	WPdyahltpr		elAaAGLYt	GigDqVqCfc	CggklnWep	cDrawseHrr	hfPnCrFV	
SEQ ID NO:24	m-xiap-3		yearIvTfGt	Wlysv..nke		qlArAGfYI	GpgDrVaCfa	CggklnWep	kDdamseHlr	hfPnCrF1	
SEQ ID NO:25	xiap-3		yearIvTfGt	Wlysv..nke		qlArAGfYI	GpgDrVaCfa	CggklnWep	kDdamseHlr	hfPnCrF1	
SEQ ID NO:26	hiap1-3		yearIvTfGt	Wlysv..nke		qlArAGfYI	GpgDrVaCfa	CggklnWep	kDdamseHlr	hfPnCrF1	
SEQ ID NO:27	hiap2-3		yearIvTfGt	Wlysv..nke		qlArAGfYI	GpgDrVaCfa	CggklnWep	kDdamseHlr	hfPnCrF1	
SEQ ID NO:28	Op_iap-2		haaRLrTfFn	WPssvlnpde		qlAaAGfYv	GnsdDvkcFg	Cdggllrcwes	gDdpwvqHak	wfPrCae1	
SEQ ID NO:29	Cp_iap-2		haaRLrTfFn	WPssvlnpde		qlAaAGfYv	GnsdDvkcFg	Cdggllrcwes	gDdpwvqHak	wfPrCae1	
SEQ ID NO:30	diap-3		haaRLrTfFn	WPssvlnpde		qlAaAGfYv	GnsdDvkcFg	Cdggllrcwes	gDdpwvqHak	wfPrCae1	
SEQ ID NO:31	diap-1		haaRLrTfFn	WPssvlnpde		qlAaAGfYv	GnsdDvkcFg	Cdggllrcwes	gDdpwvqHak	wfPrCae1	
SEQ ID NO:2	Consensus		---RL-TY--	WP-----	-----	-LA-AGFYI-	G--D-V-CF-	C-----W--	-D-----H--	--P-C-FV	



	301	BIR 3				350
cp-lap	qrpeEQMAdAG	FFYtGyGDnt	KCFyCdGGLk	dWepeDvPW	QHvrvWFdCa	
diap	qpasaLAqAG	LYYqkIGDqV	rCFhCnIGLr	swqkeDEPWf	eHAKWSPKQq	
m-xiap	VnxEQLArAG	FYalGeGDkV	KCFhCgGGLc	dWkpsEDPWd	QHAKcYPqQk	
xiap	VnxEQLArAG	FYalGeGDkV	KCFhCgGGLc	dWkpsEDPW	QHAKWYPqQk	
hiap1	VnxEQLArAG	FYYvGnsDdV	KCFcCdGGLr	cWesqDDPWv	QHAKWFPpCe	
hiap2	VnxEQLArAG	FYYvGnsDdV	KCFcCdGGLr	cWesqDDPWv	eHAKWFPpCe	
consensus	V--EQLA-AG	FYY-G-GD-V	KCF-C-GGL-	-W---DDPW-	QHAKWFP-C-	
	351					400
cp-lap	Vvq1vKGrDY	VqkVlt....	.....	.....	.....	
diap	FvllakGpaY	VseVlatta	nasscpaTap	aptlq.....	.....	
m-xiap	VlldeKQGQY	InnIhltsp.	LeEsLgrTas	kt.....	.....Ppik	
xiap	VlldeKQGQY	InnIhltsp.	LeEsLgrTas	kt.....	.....Ppik	
hiap1	VlldeKQGQY	InnIhltsp.	LeEsLgrTas	kt.....	.....Ppik	
hiap2	VlldeKQGQY	InnIhltsp.	LeEsLgrTas	kt.....	.....Ppik	
consensus	Vll--KQGQY	-----	L-E-L--T--	-----	-----P----	
	401					450
cp-lap	..acVLpge.	.....	.....	.....	.....	
diap	..adVLmdea	pakeAltLGl	dggvVrnald	rKlissGcaF	stldeLlhDi	
m-xiap	xIDdtifqnP	mVqeAirmGF	sfxdlKkime	eKIqtsGssY	lslevLIaDL	
xiap	xIDdtifqnP	mVqeAirmGF	sfxdlKkime	eKIqtsGsnY	kslevLIaDL	
hiap1	seDaVMmntP	vInaAveMGF	erslVKqtvc	rKIlalGenY	riyndIVIDL	
hiap2	seDaVMmntP	vVksAlaMGF	ndiVKqcvl	sKIlalGenY	ktvndIVsaL	
consensus	--D-V----P	-V--A--MGF	----VK----	-KI---G--Y	-----LV-DL	
	451					500
cp-lap	.....	.....	.....	.....	.....	
diap	fdcaqaaal	Evreppel...	.....	.....	.....	
m-xiap	vsAqkDnteD	E.....	.....	.....	.....	
xiap	vnAqkDsmcD	E.....	.....	.....	.....	
hiap1	InAedEireE	Ererateeke	sndililrkn	rmalfqhlac	vlpildslit	
hiap2	InAedEkreE	Ekekqaeema	sddililrkn	rmalfqhlac	vlpildslit	
consensus	--A-----	E-----	-----	-----	-----	
	501					550
cp-lap	.....	.....	.....	.....	.....	
diap	.....	.....	.....	.....	.....	
m-xiap	.....	.....	.....	.....	.....	
xiap	.....	.....	.....	.....	.....	
hiap1	aqineqend	vikqktQtsL	Qarelidtil	vkgniaatvf	mslqaeaaav	
hiap2	anvinkgend	likqktQtsL	Qarelidtil	vkgniaaana	knolkeadst	
consensus	-----	-----Q--L	Q-----	-----	-----	

				Ring Zinc Finger	500
	551				
cp-lap	...tki...	.....	.....	Ekep q veDskLCKIC yveEciVcFV	
dlap	sniskitdei	ckmsvstpnq	nlslEenRq	LxDarLCKVC LDdeEVqVVF1	
m-xlap	.....	.....	k distEEQLRR	LqEEKLSKIC MDnnIaIVF1	
xlap	.....	.....	k eistEEQLRR	LqEEKLCKIC MDnnIaIVFV	
hlap1	lyehlfvccq	ikyiptedvs	dlpveEQQLRR	LpEErtCKVC MDKEVsIVFI	
hlap2	lyknlfdvkn	mkyiptedvs	glslEEQLRR	LqEErtCKVC MDKEVsVVF1	
consensus	-----	-----	--S--EEQLRR	L--EE--LCK--C MD--EV--VF--	
	601				635
cp-lap	PCGHvVaCak	CAISVdKCPM	CRkIVtsvik	vYFS.	
dlap	PCGHLatCnq	CAPSVanCPM	CRadIkqfv	tFLS*	
m-xlap	PCGHLatCkq	CAeaVdKCPM	CytVItfnqk	IFMS*	
xlap	PCGHLVtCkq	CAeaVdKCPM	CytVItfkqk	IFMS*	
hlap1	PCGHLVvCkd	CAPslrKCPi	CRstIkqfv	tFLS*	
hlap2	PCGHLVvCqe	CAPslrKCPi	CRgIIkqfv	tFLS.	
consensus	PCGHLV-C--	CA-SV-KCPM	CR--I-----	-FLS-	

Fig. 8 (page 3 of 3)

# Alignment of RZF (Ring Zinc Finger) Domains

<b>Baculovirus</b>	
Cp_iap	Cydia pomonella
Op_ap	Orgyia pseudotsugata
<b>Human</b>	
xiap	IAP on X chromosome
hiap1, hiap2	two different human IAP genes
<b>Mouse</b>	
m-xiap	mouse homologue of human xiap gene
<b>Insect</b>	
diap	Drosophila IAP gene, not clearly a homologue of xiap or hiap

FIG. 9

## note on consensus:

The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:32	hiap2	1	EqlrrlqEer	tKVCMDkev	SVVFIPCGH1	VVCqeCApe1	rkCPiC	46
SEQ ID NO:33	hiap1		EqltrlpEer	tKVCMDkev	SVVFIPCGH1	W CKdCAPs1	rkCPiC	
SEQ ID NO:34	m-xiap		EqltrlqEek	lSKICMDmi	SVVFIPCGH1	atCkqCAeav	dkCPmC	
SEQ ID NO:35	xiap		EqltrlqEek	lCKICMDmi	SVVFIPCGH1	vtCkqCAeav	dkCPmC	
SEQ ID NO:36	diap		EenrglkDar	lCKVCLdeev	GVVFIPCGH1	atCnqCApev	anCPmC	
SEQ ID NO:37	Cp_iap		EkepqqeDsk	lCKICyveec	IVCFVPCGHV	vaCakCALsv	dkCPmC	
SEQ ID NO:38	Op_iap		aveaevaDdr	lCKIClGack	tVCFVPCGHV	vaCgkCAagv	ttCPvC	
SEQ ID NO: 1	Consensus		E-----E--	-CKICM----	-V-F-PCGH-	--C--CA---	--CP-C	

007060" E4245960

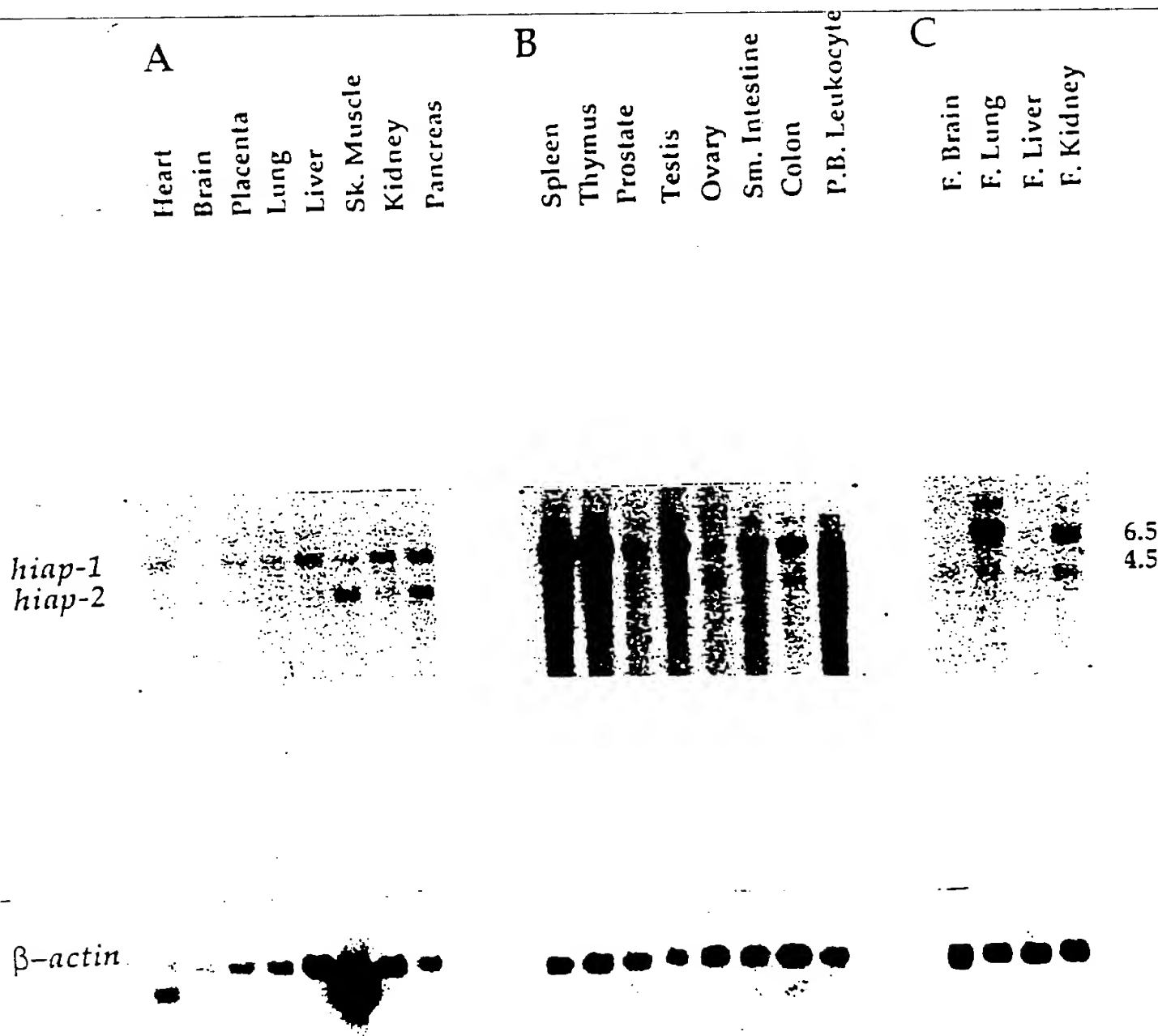


FIG. 10

007060" E4245960

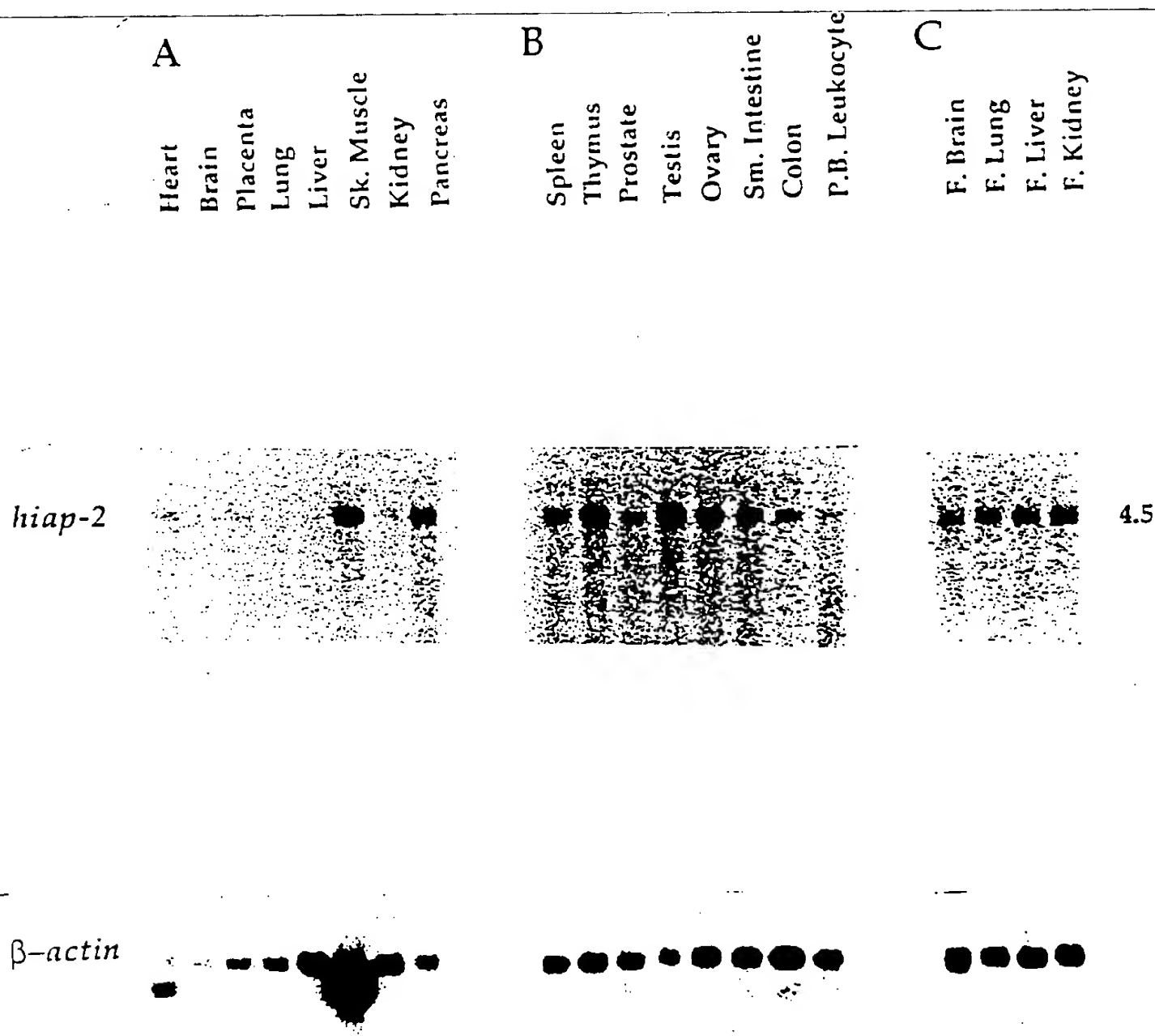


FIG. 11

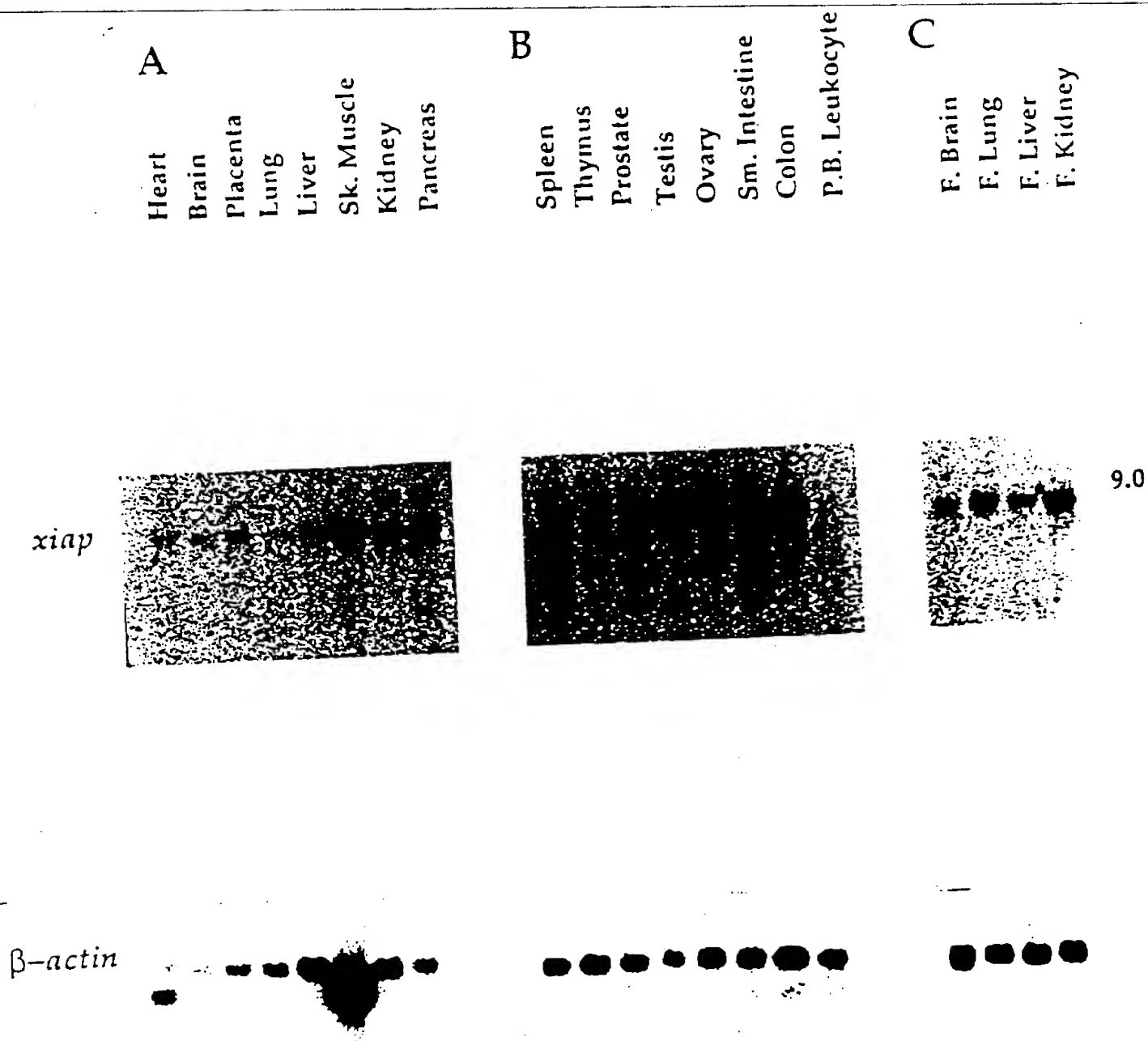
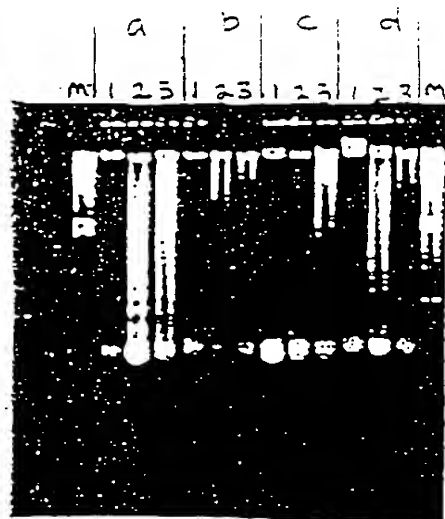


FIG. 12



00T060" E44245960

13A



13B

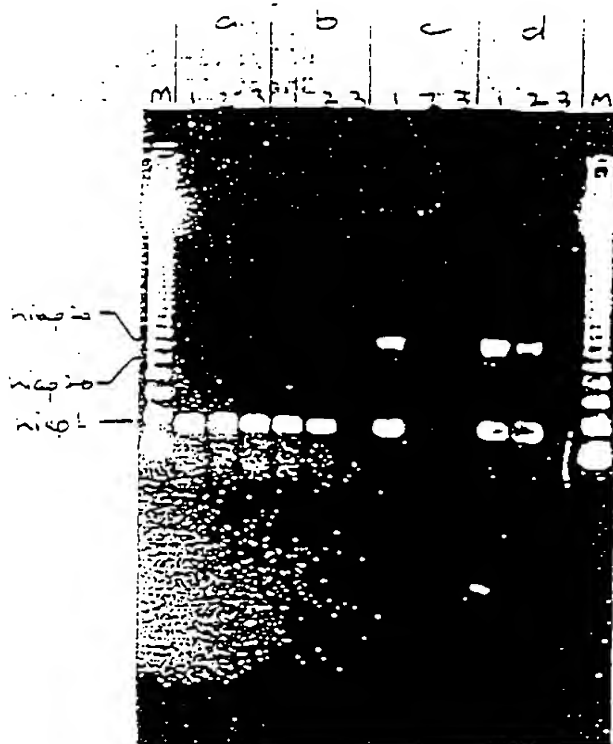
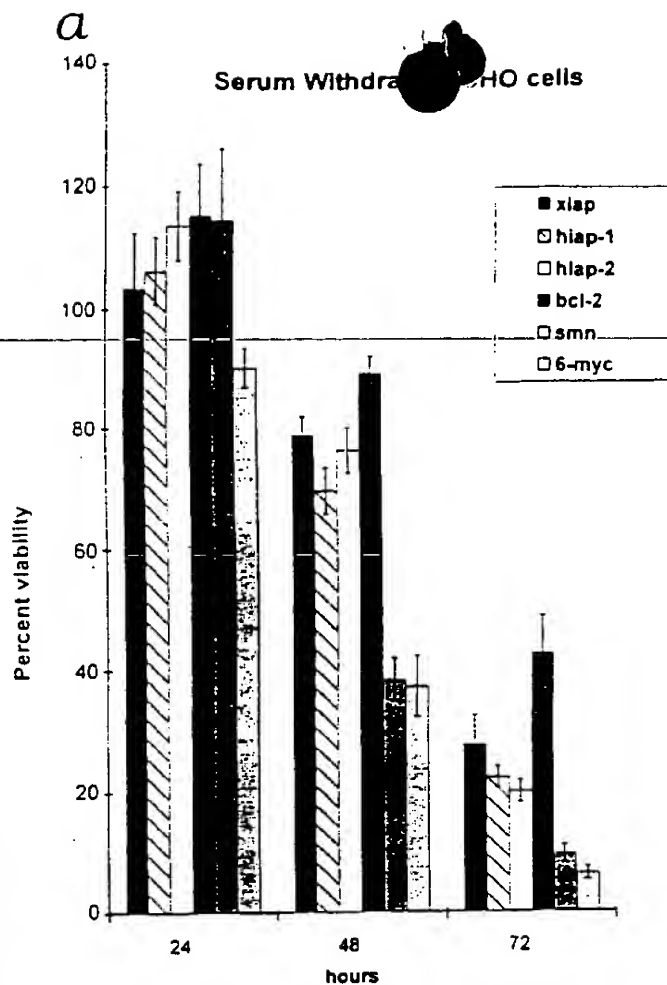
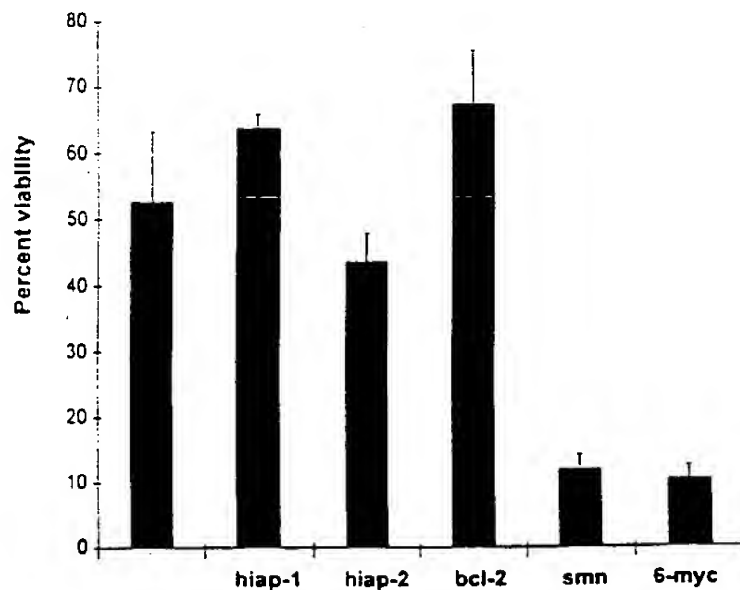


Fig. 13A and 13B



**b**

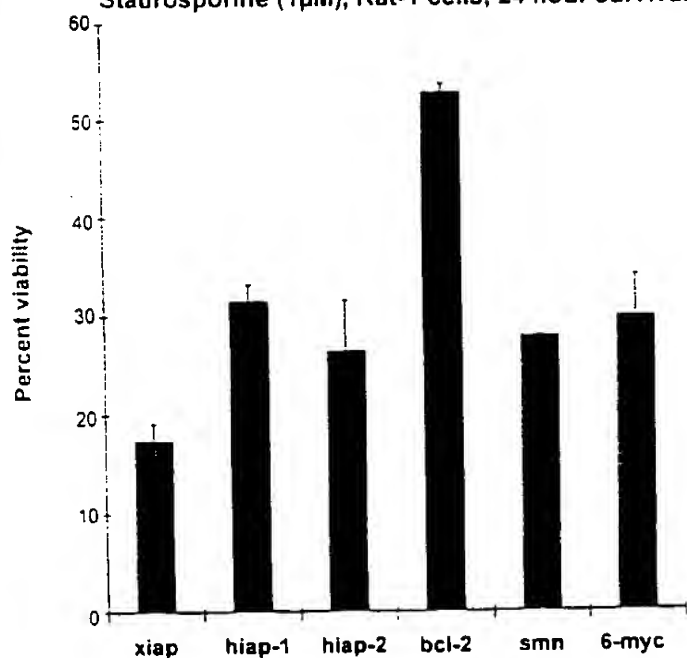
Menadione (20 $\mu$ M), CHO cells, 24 hr survival



xiap

**c**

Staurosporine (1 $\mu$ M), Rat-1 cells, 24 hour survival



**d**

Menadione (10  $\mu$ M), Rat-1 cells, 18 hour survival

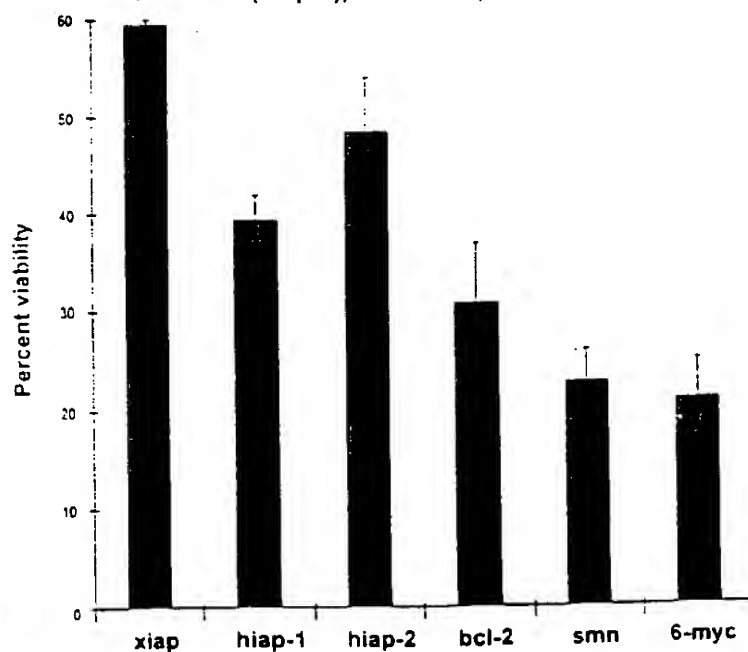


Fig. 14A - D